

GenCore version 5.1.7
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OM nucleic - nucleic search, using SW model

Run on: April 19, 2006, 21:51:30 ; Search time 260 Seconds
(without alignments)
818.622 Million cell updates/sec

Title: US-09-762-577B-11

Perfect score: 1246
Sequence: 1 cggcaggatcggtccggg.....agtggtttccctggaggt 1246

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888788028 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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4: /cgn2_6/ptodata/1/ina6B/COMB.seq: *
5: /cgn2_6/ptodata/1/inaH/COMB.seq: *
6: /cgn2_6/ptodata/1/inaPCTUS/COMB.seq: *
7: /cgn2_6/prodata/1/inaPP/COMB.seq: *
8: /cgn2_6/ptodata/1/inaRE/COMB.seq: *
9: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Score Query Match Length DB ID

Description

Result	Score	Query	Match Length	DB	ID	Description
1	1226.4	98.4	1260	3	US-09-949-016-1949	Sequence 1949, Appl
2	1162.4	93.3	1337	3	US-09-949-016-1949	Sequence 1, Appl
3	492.4	39.5	8572	3	US-09-949-016-13691	Sequence 13691, A
4	224.0	18.0	226	3	US-09-949-023-655-334	Sequence 334, App
5	204.4	16.4	3	US-09-949-016-66130	Sequence 66130, A	
6	175.2	14.1	601	3	US-09-949-016-66140	Sequence 66140, A
7	147.2	11.8	601	3	US-09-949-016-66139	Sequence 66139, A
8	135	10.8	200	3	US-09-949-016-424-216	Sequence 216, App
9	135	10.8	200	3	US-09-923-655-387	Sequence 387, App
10	111.2	8.9	601	3	US-09-949-016-66134	Sequence 66134, A
11	97	7.8	2450	3	US-09-201-916-39	Sequence 39, Appl
12	97	7.8	2450	3	US-09-001-912-39	Sequence 39, Appl
13	97	7.8	2474	3	US-09-011-356-39	Sequence 39, Appl
14	97	7.8	2474	3	US-09-672-717-226	Sequence 226, App
15	97	7.8	2676	3	US-09-210-971-11	Sequence 11, Appl
16	97	7.8	2676	3	US-08-800-912-11	Sequence 11, Appl
17	97	7.8	2676	3	US-09-617-033A-11	Sequence 11, Appl
18	88.2	7.1	601	3	US-09-949-016-66136	Sequence 66136, A
19	87.2	7.0	601	3	US-09-949-016-66138	Sequence 66138, A
20	87	7.0	601	3	US-09-949-016-66135	Sequence 66135, A
21	86.6	7.0	2862	3	US-08-569-79-13	Sequence 13, Appl
22	86.6	7.0	2862	3	US-09-689-366-13	Sequence 13, Appl
23	86.6	7.0	2862	3	US-10-332-246-13	Sequence 13, Appl
24	86.6	7.0	2862	6	PCT-US96-12860-13	Sequence 13, Appl

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11	97	7.8	2450	3	US-09-201-916-39	Sequence 39, Appl
12	97	7.8	2450	3	US-09-001-912-39	Sequence 39, Appl
13	97	7.8	2474	3	US-09-011-356-39	Sequence 39, Appl
14	97	7.8	2474	3	US-09-672-717-226	Sequence 226, App
15	97	7.8	2676	3	US-09-210-971-11	Sequence 11, Appl
16	97	7.8	2676	3	US-08-800-912-11	Sequence 11, Appl
17	97	7.8	2676	3	US-09-617-033A-11	Sequence 11, Appl
18	88.2	7.1	601	3	US-09-949-016-66136	Sequence 66136, A
19	87.2	7.0	601	3	US-09-949-016-66138	Sequence 66138, A
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24	86.6	7.0	2862	6	PCT-US96-12860-13	Sequence 13, Appl

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6: /cgn2_6/ptodata/1/inaPCTUS/COMB.seq: *
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24	86.6	7.0	2862	6	PCT-US96-12860-13	Sequence 13, Appl

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7: /cgn2_6/prodata/1/inaPP/COMB.seq: *
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9: /cgn2_6/ptodata/1/ina/backfile1.seq: *

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23	86.6	7.0	2862	3	US-10-332-246-13	Sequence 13, Appl
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

US-09-762-577B-12 (1-309) x US-09-949-016-1949 (1-1260)

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QY 61 ProLeuThrGluGluGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArglyProAla 80

Db 354 CCCCTCTAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 413

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Db 474 GCTGGAGGAGGACCCGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 533

QY 121 LysValArgCysPheCysTrpIleGlyLeuGlySerTerPlySerGlyAspAspPro 140

Db 534 AGGTGGAGGCTCTCTCTCTATGGGGCTCTGGAGCTGGAGGAGGAGGAGGAGGAGG 593

QY 141 TrpThrGluIleAlaAlaAspTerPheProSerCysGlnPhenylalanylSerTerGlyArg 160

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QY 161 AspPheValHisSerValIglnGluIleSerGlySerTerPheAspPro 180

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QY 201 LeuProThrProArgArgIleGluGlySerGluSerAlaGlyIleGluGlySerTerGly 220

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Db 489 GCGTCTCCATCT 953

QY 261 LeucInLeucysProIleCysArgAlaProValAlaGlyLeuIleGluGlySerTerGly 280

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QY 281 ***IlaArgCysIlaGluArgProGlyLeuIleSerGlyLeuProAlaProLeuCys 300

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QY 301 LeuPheTerPheThrIleAlaPheTerPheAlaCys 309

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RESULT 2

US-09-127-928-1

; Sequence 1, Application US/09127928

; Patient No. 6472172

; GENERAL INFORMATION:

; APPLICANT: Deng, Gang

; APPLICANT: Lin, Jing-Huey

APPLICANT: Morber, Michael J

TITLE OF INVENTION: DNA Encoding a No. 6472172el Human Inhibitor-of-Apoptosis

TITLE OF INVENTION: Protein

FILE REFERENCE: DNA Encoding HIAP3

CURRENT APPLICATION NUMBER: US/09/127-928

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 1

LENGTH: 1337

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (170)..(1066)

US-09-127-928-1

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Pred. No.: 1.97e-135

Length: 1337

Score: 1694.00

Matches: 308

Percent Similarity: 94.2%

Conservative: 0

Best Local Similarity: 94.2%

Mismatches: 1

Indels: 18

Query Match: 98.4%

Gaps: 1

DB:

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US-09-762-577B-12 (1-309) x US-09-127-928-1 (1-1337)

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Db 350 CCCTGAGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 409

QY 81 PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTerPheAspPro 100

Db 410 TCCCCTGACATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 469

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QY 770 CTGCCACACCCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 222

216

